

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:31:47 ; Search time 93 Seconds
(without alignments)
1207.480 Million cell updates/sec

Title: US-09-001-737-8
Perfect score: 545
Sequence: 1 MAKEIKFSADARAAWRCVD.....TPAPAMPAGMDPGMGCMG 545

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 segs, 206047115 residues

Word size : 8

Total number of hits satisfying chosen parameters: 564

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	304	55.8	481	2	033733 streptococc
2	184	33.8	184	2	0916F1 streptococc
3	156	28.6	159	2	08RJH4 streptococc
4	141	25.9	184	2	093TK8 streptococc
5	100	18.3	159	2	08RJH2 streptococc
6	91	16.7	159	2	08RJH2 streptococc
7	86	15.6	184	2	093TK4 streptococc
8	80	14.7	184	2	093TK4 streptococc
9	80	14.7	184	2	093TK4 streptococc
10	80	14.7	184	2	093TK4 streptococc
11	78	14.3	159	2	08RJH2 streptococc
12	78	14.3	184	2	093TK3 streptococc
13	78	14.3	184	2	093TK3 streptococc
14	75	13.8	184	2	093TK3 streptococc
15	70	12.8	540	2	093TK3 streptococc
16	70	12.8	540	2	093TK3 streptococc

17	67	12.3	540	2	08V758 streptococc
18	58	10.6	541	2	093E06 streptococc
19	56	10.3	542	2	09AEP7 streptococc
20	55	10.1	543	2	09KJ23 streptococc
21	47	8.6	184	2	093TK3 streptococc
22	43	7.9	184	2	093TK5 streptococc
23	36	6.6	184	2	0916F4 streptococc
24	36	6.6	184	2	0916F0 streptococc
25	36	6.6	184	2	0916E7 streptococc
26	36	6.6	184	2	0916E6 streptococc
27	36	6.6	184	2	0916F3 streptococc
28	36	6.6	184	2	093TK1 streptococc
29	36	6.6	184	2	093TK0 streptococc
30	34	6.2	184	2	09K3B7 streptococc
31	34	6.2	184	2	09K2S6 streptococc
32	34	6.2	184	2	0916F9 streptococc
33	34	6.2	184	2	0916F8 streptococc
34	34	6.2	184	2	0916F6 streptococc
35	34	6.2	184	2	0916F5 streptococc
36	33	6.1	184	2	09K2S5 streptococc
37	32	5.9	184	2	09K326 streptococc
38	32	5.9	184	2	09K2R1 streptococc
39	32	5.9	184	2	09K2O8 streptococc
40	32	5.9	184	2	0916F2 streptococc
41	32	5.9	184	2	0916F9 streptococc
42	32	5.9	184	2	0916E8 streptococc
43	32	5.9	184	2	0916F6 streptococc
44	32	5.9	184	2	0916F5 streptococc
45	32	5.9	184	2	0916F2 streptococc
46	32	5.9	184	2	0916F3 streptococc
47	32	5.9	184	2	0916F1 streptococc
48	32	5.9	184	2	0916F0 streptococc
49	32	5.9	184	2	0916F9 streptococc
50	32	5.9	184	2	0916F8 streptococc
51	32	5.9	184	2	0916F6 streptococc
52	32	5.9	184	2	0916F5 streptococc
53	32	5.9	184	2	0916F2 streptococc
54	32	5.9	184	2	0916F3 streptococc
55	31	5.7	184	2	0916F1 streptococc
56	31	5.7	184	2	0916F0 streptococc
57	31	5.7	184	2	0916F9 streptococc
58	31	5.7	184	2	0916F8 streptococc
59	31	5.7	184	2	0916F6 streptococc
60	31	5.7	184	2	0916F5 streptococc
61	31	5.7	184	2	0916F2 streptococc
62	30	5.5	184	2	0916F3 streptococc
63	30	5.5	184	2	0916F1 streptococc
64	30	5.5	184	2	0916F0 streptococc
65	30	5.5	184	2	0916F9 streptococc
66	30	5.5	184	2	0916F8 streptococc
67	29	5.3	184	2	0916F6 streptococc
68	29	5.3	184	2	0916F5 streptococc
69	28	5.1	184	2	0916F2 streptococc
70	28	5.1	184	2	0916F3 streptococc
71	28	5.1	184	2	0916F1 streptococc
72	27	5.0	184	2	0916F0 streptococc
73	26	4.8	184	2	0916F9 streptococc
74	26	4.8	184	2	0916F8 streptococc
75	26	4.8	184	2	0916F6 streptococc
76	26	4.8	184	2	0916F5 streptococc
77	26	4.8	184	2	0916F2 streptococc
78	26	4.8	184	2	0916F3 streptococc
79	26	4.8	184	2	0916F1 streptococc
80	25	4.6	184	2	0916F0 streptococc
81	25	4.6	184	2	0916F9 streptococc
82	25	4.6	184	2	0916F8 streptococc
83	25	4.6	184	2	0916F6 streptococc
84	25	4.6	184	2	0916F5 streptococc
85	25	4.6	184	2	0916F2 streptococc
86	24	4.4	184	2	0916F3 streptococc
87	24	4.4	184	2	0916F1 streptococc
88	24	4.4	184	2	0916F0 streptococc
89	24	4.4	184	2	0916F9 streptococc

90	24	4.4	543	2	09AMJ8	09amj8 anabaena sp	163	15	2.8	169	2	0930D8	0934d8 pectobacter
91	24	4.4	544	16	08Y0Z8	08ygz8 anabaena sp	164	15	2.8	169	2	0930D7	0934d7 erwina per
92	24	4.4	547	2	0936W2	093gw2 woliella r	165	15	2.8	169	2	0933Q7	0933q7 erwina pyr
93	24	4.4	547	16	0811P8	0811p8 ralsionia s	166	15	2.8	169	2	0933P4	0933p4 erwina amy
94	24	4.4	549	16	0981J9	0981j9 rhizobium l	167	15	2.8	184	2	030872	030872 staphylococ
95	24	4.4	551	16	0983S4	0983s4 rhizobium l	168	15	2.8	184	2	030872	030872 staphylococ
96	24	4.4	552	16	0984X9	0984x9 rhizobium l	169	15	2.8	184	2	095548	095548 staphylococ
97	23	4.2	417	2	0597J2	0597j2 chlamydia p	170	15	2.8	184	2	095548	095548 staphylococ
98	23	4.2	533	2	09F0S2	09f0s2 piopionibac	171	15	2.8	184	2	095548	095548 staphylococ
99	23	4.2	537	2	09F0S2	09f0s2 piopionibac	172	15	2.8	184	2	095548	095548 staphylococ
100	23	4.2	537	2	09K171	09k171 bifidobacte	173	15	2.8	184	2	095548	095548 staphylococ
101	23	4.2	540	2	09WML4	09wml4 methylovoru	174	15	2.8	184	2	095548	095548 staphylococ
102	23	4.2	541	2	09K1S7	09k1s7 gardnerella	175	15	2.8	184	2	095548	095548 staphylococ
103	23	4.2	542	2	09K1U4	09k1u4 piopionibac	176	15	2.8	184	2	095548	095548 staphylococ
104	23	4.2	542	2	09K2U4	09k2u4 bifidobacte	177	15	2.8	184	2	095548	095548 staphylococ
105	23	4.2	542	2	09K2U4	09k2u4 bifidobacte	178	15	2.8	184	2	095548	095548 staphylococ
106	22	4.0	230	2	08RNE1	08rne1 bartonella	179	15	2.8	184	2	095548	095548 staphylococ
107	22	4.0	251	2	08RNE2	08rne2 bartonella	180	15	2.8	184	2	095548	095548 staphylococ
108	22	4.0	336	2	08RNE2	08rne2 bartonella	181	15	2.8	184	2	095548	095548 staphylococ
109	22	4.0	433	2	093FX6	093fx6 bartonella	182	15	2.8	184	2	095548	095548 staphylococ
110	22	4.0	434	2	093FX5	093fx5 bartonella	183	15	2.8	184	2	095548	095548 staphylococ
111	22	4.0	436	2	085660	085660 bartonella	184	15	2.8	184	2	095548	095548 staphylococ
112	22	4.0	445	2	093FX3	093fx3 bartonella	185	15	2.8	184	2	095548	095548 staphylococ
113	22	4.0	450	2	085659	085659 bartonella	186	15	2.8	184	2	095548	095548 staphylococ
114	22	4.0	452	2	093FX8	093fx8 bartonella	187	15	2.8	184	2	095548	095548 staphylococ
115	22	4.0	454	2	093FX7	093fx7 bartonella	188	15	2.8	184	2	095548	095548 staphylococ
116	22	4.0	458	2	093FX4	093fx4 bartonella	189	15	2.8	184	2	095548	095548 staphylococ
117	22	4.0	463	2	087274	087274 bartonella	190	15	2.8	184	2	095548	095548 staphylococ
118	22	4.0	464	2	087268	087268 bartonella	191	15	2.8	184	2	095548	095548 staphylococ
119	22	4.0	467	2	093FX2	093fx2 bartonella	192	15	2.8	184	2	095548	095548 staphylococ
120	22	4.0	472	2	093FX1	093fx1 bartonella	193	15	2.8	184	2	095548	095548 staphylococ
121	22	4.0	472	2	093FX1	093fx1 bartonella	194	15	2.8	184	2	095548	095548 staphylococ
122	22	4.0	472	2	093FX1	093fx1 bartonella	195	15	2.8	184	2	095548	095548 staphylococ
123	22	4.0	474	2	087269	087269 bartonella	196	15	2.8	184	2	095548	095548 staphylococ
124	22	4.0	483	2	087270	087270 bartonella	197	15	2.8	184	2	095548	095548 staphylococ
125	22	4.0	483	2	087272	087272 bartonella	198	15	2.8	184	2	095548	095548 staphylococ
126	22	4.0	503	2	087272	087272 bartonella	199	15	2.8	184	2	095548	095548 staphylococ
127	22	4.0	502	2	087271	087271 bartonella	200	15	2.8	184	2	095548	095548 staphylococ
128	22	4.0	546	16	081691	081691 rhizobium l	201	15	2.8	184	2	095548	095548 staphylococ
129	22	4.0	539	2	081693	081693 bruceella me	202	15	2.8	184	2	095548	095548 staphylococ
130	20	3.7	539	2	P97086	P97086 tsukamurell	203	15	2.8	184	2	095548	095548 staphylococ
131	20	3.7	540	2	09AFAS	09afas tsukamurell	204	15	2.8	184	2	095548	095548 staphylococ
132	20	3.7	541	2	093Q12	093q12 corynebacte	205	15	2.8	184	2	095548	095548 staphylococ
133	20	3.7	541	2	09KGM1	09kgm1 mycobacteri	206	15	2.8	184	2	095548	095548 staphylococ
134	20	3.7	541	2	09APAS	09apas mycobacteri	207	15	2.8	184	2	095548	095548 staphylococ
135	20	3.7	542	2	09AXU5	09axu5 streptomyce	208	15	2.8	184	2	095548	095548 staphylococ
136	19	3.5	540	16	08PST7	08pst7 nocardia as	209	15	2.8	184	2	095548	095548 staphylococ
137	19	3.5	543	16	0981V5	0981v5 nocardia as	210	15	2.8	184	2	095548	095548 staphylococ
138	19	3.5	544	2	09L650	09l650 rhizobium l	211	15	2.8	184	2	095548	095548 staphylococ
139	19	3.5	546	2	09L650	09l650 rhizobium l	212	15	2.8	184	2	095548	095548 staphylococ
140	19	3.5	546	2	08R1T7	08r1t7 leptospira	213	15	2.8	184	2	095548	095548 staphylococ
141	18	3.3	444	2	08R1T7	08r1t7 xanthomonas	214	15	2.8	184	2	095548	095548 staphylococ
142	18	3.3	444	2	08R1T7	08r1t7 xanthomonas	215	15	2.8	184	2	095548	095548 staphylococ
143	18	3.3	444	2	08R1T7	08r1t7 xanthomonas	216	15	2.8	184	2	095548	095548 staphylococ
144	17	3.1	184	2	093F81	093f81 lactococcus	217	15	2.8	184	2	095548	095548 staphylococ
145	17	3.1	184	2	08VVC9	08vvc9 bacillus co	218	15	2.8	184	2	095548	095548 staphylococ
146	17	3.1	184	2	08VVC9	08vvc9 bacillus co	219	15	2.8	184	2	095548	095548 staphylococ
147	17	3.1	184	2	08VVC7	08vvc7 bacillus ps	220	15	2.8	184	2	095548	095548 staphylococ
148	17	3.1	184	2	08VVC4	08vvc4 globicatell	221	15	2.8	184	2	095548	095548 staphylococ
149	17	3.1	547	16	09PFP2	09pfp2 xyella fas	222	15	2.8	184	2	095548	095548 staphylococ
150	16	2.9	59	2	09EMD1	09emd1 streptomyce	223	15	2.8	184	2	095548	095548 staphylococ
151	16	2.9	61	2	09EUR7	09eur7 streptomyce	224	15	2.8	184	2	095548	095548 staphylococ
152	16	2.9	356	2	09K506	09k506 mycoplasma	225	15	2.8	184	2	095548	095548 staphylococ
153	16	2.9	369	2	09K503	09k503 mycoplasma	226	15	2.8	184	2	095548	095548 staphylococ
154	16	2.9	478	2	09K505	09k505 mycoplasma	227	15	2.8	184	2	095548	095548 staphylococ
155	16	2.9	548	2	087888	087888 mycoplasma	228	15	2.8	184	2	095548	095548 staphylococ
156	16	2.9	548	2	087888	087888 mycoplasma	229	15	2.8	184	2	095548	095548 staphylococ
157	15	2.8	159	2	093277	093277 mycobacteri	230	15	2.8	184	2	095548	095548 staphylococ
158	15	2.8	164	2	09X2U4	09x2u4 macrococci	231	15	2.8	184	2	095548	095548 staphylococ
159	15	2.8	167	13	08UWF4	08uwf4 staphylococ	232	15	2.8	184	2	095548	095548 staphylococ
160	15	2.8	169	2	093UH9	093uh9 erwina amy	233	15	2.8	184	2	095548	095548 staphylococ
161	15	2.8	169	2	093UH8	093uh8 erwina amy	234	15	2.8	184	2	095548	095548 staphylococ
162	15	2.8	169	2	093UH7	093uh7 erwina pyr	235	15	2.8	184	2	095548	095548 staphylococ

236	15	2.8	563	4	096F26	096f26 homo sapien	309	13	2.4	546	2	08RNU2	08rnu2 helicobacter
237	15	2.8	573	5	0905N2	0905n2 myzus persi	310	13	2.4	565	5	09BLG8	09blg8 paramecium
238	15	2.8	581	5	046219	046219 culicoides	311	13	2.4	575	5	09YI08	09yi08 toxoplasma
239	15	2.8	582	5	0905L7	0905l7 paracetrot	312	13	2.4	596	10	09FHA9	09fha9 arabidopsis
240	15	2.8	598	5	090X77	090x77 onchocerca	313	13	2.4	566	10	09LJE4	09lje4 arabidopsis
241	14	2.6	82	2	09FAF1	09faf1 buchnera ap	314	13	2.4	599	10	09SAV2	09sav2 solanum tub
242	14	2.6	82	2	09FAF1	09faf1 buchnera ap	315	13	2.4	600	10	09SAV2	09sav2 arabidopsis
243	14	2.6	82	2	09FAE9	09fae9 buchnera ap	316	13	2.4	601	10	09LMT6	09lmt6 oryza sativ
244	14	2.6	82	2	09FAE7	09fae7 buchnera ap	317	13	2.4	172	5	09S1G6	09s1g6 tetrahymena
245	14	2.6	82	2	09FAE5	09fae5 buchnera ap	318	13	2.2	184	2	09XZ00	09xz00 staphylococ
246	14	2.6	82	2	09FAE3	09fae3 buchnera ap	319	13	2.2	185	2	09XZ00	09xz00 staphylococ
247	14	2.6	82	2	09FAE3	09fae3 buchnera ap	319	13	2.2	185	2	09XZ00	09xz00 staphylococ
248	14	2.6	536	2	09VUS2	09vus2 secondary s	320	12	2.2	185	2	09XZ00	09xz00 staphylococ
249	14	2.6	536	2	09VUS2	09vus2 secondary s	320	12	2.2	185	2	09XZ00	09xz00 staphylococ
250	14	2.6	536	2	09VUS2	09vus2 secondary s	320	12	2.2	185	2	09XZ00	09xz00 staphylococ
251	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
252	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
253	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
254	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
255	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
256	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
257	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
258	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
259	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
260	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
261	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
262	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
263	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
264	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
265	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
266	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
267	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
268	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
269	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
270	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
271	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
272	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
273	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
274	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
275	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
276	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
277	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
278	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
279	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
280	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
281	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
282	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
283	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
284	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
285	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
286	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
287	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
288	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
289	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
290	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
291	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
292	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
293	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
294	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
295	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
296	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
297	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
298	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
299	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
300	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
301	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
302	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
303	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
304	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
305	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
306	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
307	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp
308	14	2.6	550	2	09ESV1	09esv1 thermotoga	321	12	2.2	356	2	08VVC5	08vvc5 anaerobiosp

382	11	2.0	124	2	09AE4	09AE4 mycobacteri	455	11	2.0	184	2	034818	034818 staphylococ
383	11	2.0	125	2	09AE2	09AE2 mycobacteri	456	11	2.0	184	2	034972	034972 staphylococ
384	11	2.0	126	2	09LB5	09LB5 mycobacteri	457	11	2.0	186	2	08VV0	08VV0 flavobacter
385	11	2.0	127	2	09FW1	09FW1 mycobacteri	458	11	2.0	186	2	08VV7	08VV7 chrysobact
386	11	2.0	127	2	09AE9	09AE9 mycobacteri	459	11	2.0	186	2	08VJ7	08VJ7 bartgeella
387	11	2.0	127	2	09AEC5	09AEC5 mycobacteri	460	11	2.0	196	2	09K15	09K15 bifidobacte
388	11	2.0	127	2	09KH5	09KH5 mycobacteri	461	11	2.0	196	2	09K16	09K16 bifidobacte
389	11	2.0	128	2	09AEX4	09AEX4 mycobacteri	462	11	2.0	196	2	09AGE4	09AGE4 bifidobacte
390	11	2.0	128	2	09AEX3	09AEX3 mycobacteri	463	11	2.0	196	2	09EVR4	09EVR4 flavobacter
391	11	2.0	129	2	09AEC2	09AEC2 mycobacteri	464	11	2.0	196	2	09EVR3	09EVR3 bifidobacte
392	11	2.0	130	10	09AEC3	09AEC3 mycobacteri	465	11	2.0	223	5	09U3B0	09U3B0 caenorhabd
393	11	2.0	132	2	09AE98	09AE98 mycobacteri	466	11	2.0	258	4	09K13	09K13 homo sapien
394	11	2.0	132	2	08RMX6	08RMX6 mycobacteri	467	11	2.0	315	5	09AIR9	09AIR9 aster yell
395	11	2.0	133	2	09ZH66	09ZH66 mycobacteri	468	11	2.0	343	5	076781	076781 cryptospor
396	11	2.0	133	2	09AEC4	09AEC4 mycobacteri	469	11	2.0	501	5	061118	061118 leishmania
397	11	2.0	133	2	09AEC0	09AEC0 mycobacteri	470	11	2.0	544	5	P90622	P90622 trichomonas
398	11	2.0	133	2	09AEB5	09AEB5 mycobacteri	471	11	2.0	560	16	08VVS8	08VVS8 anaplasma sp
399	11	2.0	133	2	09GL3	09GL3 mycobacteri	472	11	2.0	566	5	097130	097130 leishmania
400	11	2.0	133	2	08WM17	08WM17 mycobacteri	473	11	2.0	594	5	097131	097131 leishmania
401	11	2.0	133	2	08WM16	08WM16 mycobacteri	474	11	2.0	639	5	08V1V0	08V1V0 diosiphila
402	11	2.0	133	2	08WM15	08WM15 mycobacteri	475	11	2.0	45	5	08VW6	08VW6 myzus persi
403	11	2.0	133	2	08WM14	08WM14 mycobacteri	476	11	1.8	194	2	09K170	09K170 bifidobacte
404	11	2.0	133	2	08WM13	08WM13 mycobacteri	477	11	1.8	196	2	09K160	09K160 bifidobacte
405	11	2.0	133	2	08WM12	08WM12 mycobacteri	478	11	1.8	196	2	09K169	09K169 bifidobacte
406	11	2.0	133	2	08WM11	08WM11 mycobacteri	479	11	1.8	196	2	09K168	09K168 bifidobacte
407	11	2.0	133	2	08WM10	08WM10 mycobacteri	480	11	1.8	196	2	09K167	09K167 bifidobacte
408	11	2.0	133	2	08WM09	08WM09 mycobacteri	481	11	1.8	196	2	09K166	09K166 bifidobacte
409	11	2.0	133	2	08R460	08R460 mycobacteri	482	11	1.8	196	2	09K165	09K165 bifidobacte
410	11	2.0	133	2	09R458	09R458 mycobacteri	483	11	1.8	196	2	09K164	09K164 bifidobacte
411	11	2.0	133	2	09ZHE7	09ZHE7 mycobacteri	484	11	1.8	196	2	09K163	09K163 bifidobacte
412	11	2.0	133	2	09ZHE6	09ZHE6 mycobacteri	485	11	1.8	196	2	09K162	09K162 bifidobacte
413	11	2.0	133	2	09ZHE5	09ZHE5 mycobacteri	486	11	1.8	196	2	09K159	09K159 bifidobacte
414	11	2.0	133	2	09ZHE4	09ZHE4 mycobacteri	487	11	1.8	196	2	09K158	09K158 bifidobacte
415	11	2.0	133	2	09ZHE3	09ZHE3 mycobacteri	488	11	1.8	196	2	09ZEM1	09ZEM1 bifidobacte
416	11	2.0	133	2	09ZHE2	09ZHE2 mycobacteri	489	11	1.8	196	2	09EX82	09EX82 bifidobacte
417	11	2.0	133	2	09S636	09S636 mycobacteri	490	11	1.8	196	2	09EX81	09EX81 bifidobacte
418	11	2.0	133	2	09S635	09S635 mycobacteri	491	11	1.8	196	2	09EX80	09EX80 bifidobacte
419	11	2.0	133	2	09S634	09S634 mycobacteri	492	11	1.8	196	2	09EX79	09EX79 bifidobacte
420	11	2.0	133	2	09S633	09S633 mycobacteri	493	11	1.8	196	2	09EX78	09EX78 bifidobacte
421	11	2.0	134	2	09AE9	09AE9 mycobacteri	494	11	1.8	196	2	09EX77	09EX77 bifidobacte
422	11	2.0	134	2	09AE8	09AE8 mycobacteri	495	11	1.8	196	2	09EX76	09EX76 bifidobacte
423	11	2.0	134	2	09AE94	09AE94 mycobacteri	496	11	1.8	196	2	09EX75	09EX75 bifidobacte
424	11	2.0	134	2	09AE91	09AE91 mycobacteri	497	11	1.8	196	2	09EX74	09EX74 bifidobacte
425	11	2.0	134	2	09AE89	09AE89 mycobacteri	498	11	1.8	196	2	09EX73	09EX73 bifidobacte
426	11	2.0	135	2	09AE88	09AE88 mycobacteri	499	11	1.8	196	2	09EX72	09EX72 bifidobacte
427	11	2.0	135	2	09AE86	09AE86 mycobacteri	500	11	1.8	197	2	09K167	09K167 bifidobacte
428	11	2.0	136	2	09AE99	09AE99 mycobacteri	501	11	1.8	197	2	09EX72	09EX72 bifidobacte
429	11	2.0	137	2	09AE82	09AE82 mycobacteri	502	11	1.8	197	2	09EX71	09EX71 bifidobacte
430	11	2.0	137	2	09AE97	09AE97 mycobacteri	503	11	1.8	220	4	09K164	09K164 delnococcus
431	11	2.0	138	2	09AE93	09AE93 mycobacteri	504	11	1.8	228	2	09K162	09K162 delnococcus
432	11	2.0	139	2	09AE93	09AE93 mycobacteri	505	11	1.8	239	2	09K161	09K161 delnococcus
433	11	2.0	140	2	09AE93	09AE93 mycobacteri	506	11	1.8	259	2	09K160	09K160 delnococcus
434	11	2.0	141	2	09AC92	09AC92 mycobacteri	507	11	1.8	259	2	09K159	09K159 delnococcus
435	11	2.0	141	2	09AC92	09AC92 mycobacteri	508	11	1.8	259	2	09K158	09K158 delnococcus
436	11	2.0	145	2	09AEB0	09AEB0 mycobacteri	509	11	1.8	262	2	09K157	09K157 delnococcus
437	11	2.0	145	2	09AEB1	09AEB1 mycobacteri	510	11	1.8	262	2	09K156	09K156 delnococcus
438	11	2.0	146	2	09AEB1	09AEB1 mycobacteri	511	11	1.8	271	3	09K155	09K155 delnococcus
439	11	2.0	147	2	09K209	09K209 mycobacteri	512	11	1.8	360	3	09K154	09K154 delnococcus
440	11	2.0	147	2	09K209	09K209 mycobacteri	513	11	1.8	524	10	09K153	09K153 delnococcus
441	11	2.0	147	2	09AEB7	09AEB7 mycobacteri	514	11	1.8	556	5	09K152	09K152 delnococcus
442	11	2.0	147	2	09AEB5	09AEB5 mycobacteri	515	11	1.8	577	5	09K151	09K151 delnococcus
443	11	2.0	147	2	09AEB8	09AEB8 mycobacteri	516	11	1.8	579	5	09K150	09K150 delnococcus
444	11	2.0	147	2	09AEB4	09AEB4 mycobacteri	517	11	1.8	584	10	09K149	09K149 delnococcus
445	11	2.0	147	2	09AEB3	09AEB3 mycobacteri	518	11	1.8	33	2	09K148	09K148 delnococcus
446	11	2.0	148	2	09AEB6	09AEB6 mycobacteri	519	11	1.8	48	10	09K147	09K147 delnococcus
447	11	2.0	172	5	09B165	09B165 mycobacteri	520	11	1.8	115	5	09K146	09K146 delnococcus
448	11	2.0	172	5	09B165	09B165 mycobacteri	521	11	1.8	146	2	09K145	09K145 delnococcus
449	11	2.0	175	5	09B165	09B165 mycobacteri	522	11	1.8	146	2	09K144	09K144 delnococcus
450	11	2.0	184	2	09K2N8	09K2N8 mycobacteri	523	11	1.8	186	2	09K143	09K143 delnococcus
451	11	2.0	184	2	09K2N8	09K2N8 mycobacteri	524	11	1.8	220	16	09K142	09K142 delnococcus
452	11	2.0	184	2	09K2N8	09K2N8 mycobacteri	525	11	1.8	361	5	09K141	09K141 delnococcus
453	11	2.0	184	2	09K2N8	09K2N8 mycobacteri	526	11	1.8	512	5	09K140	09K140 delnococcus
454	11	2.0	184	2	09K2N8	09K2N8 mycobacteri	527	11	1.8	558	5	09K139	09K139 delnococcus

528	9	1.7	580	5	096783	096783 plectus acu
529	8	1.5	44	097273	097273 brassica na	
530	8	1.5	98	097652	097652 mycobacteri	
531	8	1.5	131	097651	097651 xyliella fas	
532	8	1.5	146	097671	097671 methanosarc	
533	8	1.5	156	097681	097681 agrobacteri	
534	8	1.5	161	094421	094421 haemophilus	
535	8	1.5	180	094789	094789 leifsonia a	
536	8	1.5	184	095537	095537 staphylococ	
537	8	1.5	184	095201	095201 staphylococ	
538	8	1.5	191	093553	093553 neisseria m	
539	8	1.5	197	098402	098402 rhizobium l	
540	8	1.5	235	097261	097261 rhizobium m	
541	8	1.5	326	097615	097615 avicenna m	
542	8	1.5	333	097659	097659 agrobacteri	
543	8	1.5	343	097659	097659 agrobacteri	
544	8	1.5	366	097659	097659 agrobacteri	
545	8	1.5	391	097659	097659 agrobacteri	
546	8	1.5	429	097659	097659 agrobacteri	
547	8	1.5	431	097659	097659 agrobacteri	
548	8	1.5	440	097659	097659 agrobacteri	
549	8	1.5	473	097659	097659 agrobacteri	
550	8	1.5	524	097659	097659 agrobacteri	
551	8	1.5	536	097659	097659 agrobacteri	
552	8	1.5	538	097659	097659 agrobacteri	
553	8	1.5	544	097659	097659 agrobacteri	
554	8	1.5	549	097659	097659 agrobacteri	
555	8	1.5	549	097659	097659 agrobacteri	
556	8	1.5	549	097659	097659 agrobacteri	
557	8	1.5	549	097659	097659 agrobacteri	
558	8	1.5	549	097659	097659 agrobacteri	
559	8	1.5	549	097659	097659 agrobacteri	
560	8	1.5	549	097659	097659 agrobacteri	
561	8	1.5	549	097659	097659 agrobacteri	
562	8	1.5	549	097659	097659 agrobacteri	
563	8	1.5	549	097659	097659 agrobacteri	
564	8	1.5	549	097659	097659 agrobacteri	

ALIGNMENTS

RESULT 1						
ID	033733	PRELIMINARY:	PRT:	481 AA.		
AC	033733:					
DT	01-JAN-1998 (TRENBLREL. 05, Created)					
DT	01-JAN-1998 (TRENBLREL. 05, Last sequence update)					
DT	01-MAR-2002 (TRENBLREL. 20, Last annotation update)					
DE	60 kDa chaperonin (Protein Cpn60) (GroEL protein) (Fragment).					
GN	GROEL.					
OS	Streptococcus pyogenes.					
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;					
OC	Streptococcaceae; Streptococcus.					
OX	NCBI_TaxID=1314;					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=SEROTYPE M49.					
RA	Pohl B., Podilelski A., Zarges I.;					
RL	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.					
CC	-1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND					
CC	PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS					
CC	CONDITIONS (BY SIMILARITY).					
CC	-1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF					
CC	7 SUBUNITS (BY SIMILARITY).					
CC	-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.					
CC	EMBL: X89236; CA61520.1;					
DR	HSP: P06139; IGR.					
DR	InterPro: IPR001844; Chaperonin_Cpn60.					
DR	InterPro: IPR002423; Cpn60_TCP-1.					
DR	Pfam: PF00118; Cpn60_TCP1.1.					
DR	PRINTS: PR00298; CHAPERONIN60.					
DR	PRINTS: PR00304; TCOMPLEXTCP1.					

DR	PROSITE; P500296; CHAPERONIN_CPN60.1.					
KW	ATP-binding; Chaperone.					
FT	NON_TER					
SEQUENCE	481 AA; 50496 MW; FA080B97CA7B6D11 CRC6;					
Query Match	55.8%; Score 304; DB 2; Length					
Best Local Similarity	100.0%; Pred. No. 2,4e-304;					
Matches 304; Conservative 0; Mismatches 0; Ind						
222	DKKSNIDILPLLEEVLTNRPPLIADVDGEALPTLVLRKSTGVVAVKAPGCD	281				
Db	160 DKKSNIDILPLLEEVLTNRPPLIADVDGEALPTLVLRKSTGVVAVKAPGCD	219				
QY	282 RRRKMEADIALTGGVITLEDGLKDATMTALGAKITVDKSTVIVEDSSSEAIA	341				
Db	220 RRRKMEADIALTGGVITLEDGLKDATMTALGAKITVDKSTVIVEDSSSEAIA	279				
QY	342 NRALIKSOLETTTSDPFRKLOERLAKGAVAVIKVAPETALKEKRLIDALNAT	401				
Db	280 NRALIKSOLETTTSDPFRKLOERLAKGAVAVIKVAPETALKEKRLIDALNAT	339				
QY	402 RAAVEGIYAGGTALITVIEKVALEEGDDATGNIVLRALPEPVQIALNGYEGSV	461				
Db	340 RAAVEGIYAGGTALITVIEKVALEEGDDATGNIVLRALPEPVQIALNGYEGSV	399				
QY	462 VIKLKNRPAGTGFNAAGENVDMIKTGIIDPVKVRSAALQNAASVASLITTEAVVANK	521				
Db	400 VIKLKNRPAGTGFNAAGENVDMIKTGIIDPVKVRSAALQNAASVASLITTEAVVANK	459				
QY	522 PEPA 525					
Db	460 PEPA 463					

RESULT 2						
ID	09L6F1	PRELIMINARY:	PRT:	184 AA.		
AC	09L6F1:					
DT	01-OCT-2000 (TRENBLREL. 15, Created)					
DT	01-OCT-2000 (TRENBLREL. 15, Last sequence update)					
DT	01-MAR-2002 (TRENBLREL. 20, Last annotation update)					
DE	Cpn60 (Fragment).					
GN	CPN60.					
OS	Streptococcus pyogenes.					
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;					
OC	Streptococcaceae; Streptococcus.					
OX	NCBI_TaxID=1314;					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=ATCC19615.					
RA	Goh S.-H., Hill J.E., Hemmingsen S.M.;					
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.					
CC	EMBL: AF32806; AAK48857.1;					
DR	HSP: P45746; IGRV.					
DR	InterPro: IPR002423; Cpn60_TCP-1.					
DR	Pfam: PF00118; Cpn60_TCP1.1.					
FT	ATP-binding; Chaperone.					
FT	NON_TER					
SO	SEQUENCE 184 AA; 19819 MW; 27C23787A267C1F8 CRC64;					
Query Match	33.8%; Score 184; DB 2; Length 184;					
Best Local Similarity	100.0%; Pred. No. 6e-181;					
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						

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OY 91 ATVLTQAIHHEGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAAS 150
DB 1 ATVLTQAIHHEGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAAS 60
OY 151 SRSKVGGEYISEAMERVNDGVITTEESRGHETELEVVEGMDRGYLSQYVTDNEKV 210
DB 61 SRSKVGGEYISEAMERVNDGVITTEESRGHETELEVVEGMDRGYLSQYVTDNEKV 120
OY 211 ADLENPFLITDKKVSNIODILPLEEVLKTNRPILLIADVDGEALPTLVINKRTGFN 270
DB 121 ADLENPFLITDKKVSNIODILPLEEVLKTNRPILLIADVDGEALPTLVINKRTGFN 180
OY 271 VYAV 274
DB 181 VYAV 184

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RESULT 3

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OY 08RJH4 PRELIMINARY; PRT; 159 AA.
DB 08RJH4
AC 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 60 kDa chaparonin Cpn60 (Fragment).
CN Cpn60.
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OX Streptococcaceae; Streptococcus.
RN NCBL_TaxID-1334;
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27957, ATCC 43078, 62, AND 74;
RA McDonald W.L., Deighton M.A., Fry B.N.;
RT "Phylogeny comparison of Streptococcus sp. associated with bovine mastitis using 16S rRNA and newly sequenced HSP60 genes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF485794; AAL96573.1; -
DR EMBL: AF485795; AAL96574.1; -
DR EMBL: AF485796; AAL96575.1; -
DR EMBL: AF485797; AAL96576.1; -
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 17216 MW; 079B14AF907433BE CRC64;

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Query Match 28.6%; Score 156; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 4e-152;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 101 EGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAASRSKVGGEYI 160
DB 4 EGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAASRSKVGGEYI 63
OY 161 SEAMERVNDGVITTEESRGHETELEVVEGMDRGYLSQYVTDNEKVADLENPFLIT 220
DB 64 SEAMERVNDGVITTEESRGHETELEVVEGMDRGYLSQYVTDNEKVADLENPFLIT 123
OY 221 TDKKVSNIODILPLEEVLKTNRPILLIADVDGEA 236
DB 124 TDKKVSNIODILPLEEVLKTNRPILLIADVDGEA 159

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RESULT 4

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OY 093TK8 PRELIMINARY; PRT; 184 AA.
DB 093TK8
AC 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
CN Cpn60 (Fragment).
OS Streptococcus canis.

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OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBL_TaxID-1329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC43496;
RA Goh S.H., Hill J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352804; AAK4885.1; -
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; cpn60_TCF1; 1.
KW ATP-binding; Chaparone.
FT NON_TER 1
FT NON_TER 184
SQ SEQUENCE 184 AA; 19768 MW; 479C981163B1166E CRC64;

```

Query Match 25.9%; Score 141; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.4e-136;
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 101 EGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAASRSKVGGEYI 160
DB 11 EGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAASRSKVGGEYI 70
OY 161 SEAMERVNDGVITTEESRGHETELEVVEGMDRGYLSQYVTDNEKVADLENPFLIT 220
DB 71 SEAMERVNDGVITTEESRGHETELEVVEGMDRGYLSQYVTDNEKVADLENPFLIT 130
OY 221 TDKKVSNIODILPLEEVLKTNRPILLIADVDGEA 236
DB 131 TDKKVSNIODILPLEEVLKTNRPILLIADVDGEA 151

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RESULT 5

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OY 08RJ42 PRELIMINARY; PRT; 159 AA.
DB 08RJ42
AC 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 60 kDa chaparonin Cpn60 (Fragment).
CN Cpn60.
OS Streptococcus uberis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OX Streptococcaceae; Streptococcus.
RN NCBL_TaxID-1349;
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13387, ATCC 700407, 16, AND 33;
RA McDonald W.L., Deighton M.A., Fry B.N.;
RT "Phylogeny comparison of Streptococcus sp. associated with bovine mastitis using 16S rRNA and newly sequenced HSP60 genes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF485801; AAL96580.1; -
DR EMBL: AF485802; AAL96581.1; -
DR EMBL: AF485803; AAL96582.1; -
DR EMBL: AF485804; AAL96583.1; -
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 17275 MW; 9C456169FEC22AF CRC64;

```

Query Match 18.3%; Score 100; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 2.4e-94;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 130 LKAIAPVSGKEAIAQVAASRSKVGGEYISEAMERVNDGVITTEESRGHETELEVVE 189
DB 33 LKAIAPVSGKEAIAQVAASRSKVGGEYISEAMERVNDGVITTEESRGHETELEVVE 92
OY 190 GMDRGYLSQYVTDNEKVADLENPFLITDKKVSNIQ 229
DB 93 GMDRGYLSQYVTDNEKVADLENPFLITDKKVSNIQ 132

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RESULT 6
08RJG8      PRELIMINARY:      PRT:      159 AA.
ID 08RJG8;
AC 08RJG8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 60 kDa chaperonin Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus parauberis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1348;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13386, 21B, AND 25;
RA McDonald M.L., Deighton M.A., Fry B.N.;
RT "Phylogeny comparison of Streptococcus sp. associated with bovine
RT mastitis using 16S rRNA and newly sequenced HSP60 genes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF485798; AAL96577.1;
DR EMBL: AF485799; AAL96578.1;
DR EMBL: AF485800; AAL96579.1;
FT NON_TER      1
FT SEQUENCE      159 AA; 17313 MW; 110382BF8F70EFD CRC64;
SQ
Query Match      16.7%; Score 91; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 4,6e-85;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 GKFAIAOVAAVSSRSKGEYISEAMERVNDGYITIEESRGHETELEVESGMPDRGYL 198
DB 42 GKFAIAOVAAVSSRSKGEYISEAMERVNDGYITIEESRGHETELEVESGMPDRGYL 101
QY 199 SOYVWTDNEKRVADLENPFILITDKKYSNIO 229
DB 102 SOYVWTDNEKRVADLENPFILITDKKYSNIO 132

RESULT 7
093TK4      PRELIMINARY:      PRT:      184 AA.
ID 093TK4;
AC 093TK4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus porcinus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC43138;
RA Goh S.H., Hill J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352810; AAK48861.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
KW ATP-binding; Chaperone.
FT NON_TER      1
FT SEQUENCE      184 AA; 19868 MW; DE048E8708C36177 CRC64;
SQ
Query Match      15.8%; Score 86; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 7,5e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 139 GKFAIAOVAAVSSRSKGEYISEAMERVNDGYITIEESRGHETELEVESGMPDRGYL 198
DB 49 GKFAIAOVAAVSSRSKGEYISEAMERVNDGYITIEESRGHETELEVESGMPDRGYL 108
QY 199 SOYVWTDNEKRVADLENPFILITDKK 224
DB 109 SOYVWTDNEKRVADLENPFILITDKK 134

RESULT 8
093TL2      PRELIMINARY:      PRT:      184 AA.
ID 093TL2;
AC 093TL2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC19258;
RA Goh S.H., Hill J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352800; AAK48851.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
KW ATP-binding; Chaperone.
FT NON_TER      1
FT SEQUENCE      184 AA; 19848 MW; ECC6BD9A5FAF745A CRC64;
SQ
Query Match      14.7%; Score 80; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1,2e-73;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 KEAIAOVAAVSSRSKGEYISEAMERVNDGYITIEESRGHETELEVESGMPDRGYL 199
DB 50 KEAIAOVAAVSSRSKGEYISEAMERVNDGYITIEESRGHETELEVESGMPDRGYL 109
QY 200 QYVWTDNEKRVADLENPFIL 219
DB 110 QYVWTDNEKRVADLENPFIL 129

RESULT 9
093TK9      PRELIMINARY:      PRT:      184 AA.
ID 093TK9;
AC 093TK9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus vestibularis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC49124;
RA Goh S.H., Hill J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352803; AAK48854.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
KW ATP-binding; Chaperone.
FT NON_TER      1

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FT NON_TER 184 184
SQ SEQUENCE 184 AA; 19864 MW; 8234EDBE164FC988 CRC64;

Query Match
Best Local Similarity 14.7%; Score 80; DB 2; Length 184;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 KEAIAOVAVSSRSKGEYISEAMERVNDGVITTEESRGMETELEVVEGMDRGYLS 199
DB 50 KEAIAOVAVSSRSKGEYISEAMERVNDGVITTEESRGMETELEVVEGMDRGYLS 109
QY 200 QYVTDNEKRVADLENPFIL 219
DB 110 QYVTDNEKRVADLENPFIL 129

RESULT 10
Q93TK7 PRELIMINARY; PRT; 184 AA.
AC Q93TK7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus salivarius.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1304;
RN [1]
RP SEQUENCE FROM N.A.
RA Goh S.H., Hall J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352807; AAK48858.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
KW ATP-binding; Chapterone.
FT NON_TER 1 184
FT SEQUENCE 184 AA; 19864 MW; 8234EDBE164FC988 CRC64;

Query Match
Best Local Similarity 14.7%; Score 80; DB 2; Length 184;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 KEAIAOVAVSSRSKGEYISEAMERVNDGVITTEESRGMETELEVVEGMDRGYLS 199
DB 50 KEAIAOVAVSSRSKGEYISEAMERVNDGVITTEESRGMETELEVVEGMDRGYLS 109
QY 200 QYVTDNEKRVADLENPFIL 219
DB 110 QYVTDNEKRVADLENPFIL 129

RESULT 11
Q8RJ02 PRELIMINARY; PRT; 159 AA.
AC Q8RJ02;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 60 kDa chaperonin Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1311;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-ATCC 13813, ATCC 27956, 13821-4, AND 13824-5;
RA McDonald W.L., Deligton M.A., Fry B.N.;

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RT "Phylogeny comparison of Streptococcus sp. associated with bovine
RT mastitis using 16S rRNA and newly sequenced HRP60 genes.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF485790; AAL96569.1;
DR EMBL: AF485791; AAL96570.1;
DR EMBL: AF485792; AAL96571.1;
DR EMBL: AF485793; AAL96572.1;
FT NON_TER 1 159
FT SEQUENCE 159 AA; 17391 MW; C6F4C7AB753864C CRC64;

Query Match
Best Local Similarity 14.3%; Score 78; DB 2; Length 159;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 IAQPVSGKEAIAOVAVSSRSKGEYISEAMERVNDGVITTEESRGMETELEVVEGMD 192
DB 36 IAQPVSGKEAIAOVAVSSRSKGEYISEAMERVNDGVITTEESRGMETELEVVEGMD 95
QY 193 FDRGYLSQVYVTDNEKRV 210
DB 96 FDRGYLSQVYVTDNEKRV 113

RESULT 12
Q93TK3 PRELIMINARY; PRT; 184 AA.
AC Q93TK3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1311;
RN [1]
RP SEQUENCE FROM N.A.
RA Goh S.H., Hall J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352811; AAK48862.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
KW ATP-binding; Chapterone.
FT NON_TER 1 184
FT SEQUENCE 184 AA; 20012 MW; D420BAEB24EBDFB CRC64;

Query Match
Best Local Similarity 14.3%; Score 78; DB 2; Length 184;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 IAQPVSGKEAIAOVAVSSRSKGEYISEAMERVNDGVITTEESRGMETELEVVEGMD 192
DB 43 IAQPVSGKEAIAOVAVSSRSKGEYISEAMERVNDGVITTEESRGMETELEVVEGMD 102
QY 193 FDRGYLSQVYVTDNEKRV 210
DB 103 FDRGYLSQVYVTDNEKRV 120

RESULT 13
Q9AME7 PRELIMINARY; PRT; 540 AA.
AC Q9AME7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
OS Streptococcus agalactiae.

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OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1311;
RN [1]
RP SEQUENCE FROM N.A.
RA Jwo-Farn C.;
RT *Cloning, sequencing, and characterization of 60 kDa Chaperonin gene
RT from Streptococcus agalactiae. *;
RL submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AF325222; AAK12938.1; -;
DR HSP: P06139; 1GRL.
DR InterPro: IPR001844; Chaperln_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PROSITE: PS00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONIN60_CPN60; 1.
KM ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 57287 MW; F392085FCF919DD1 CRC64;

Query Match 14.3%; Score 78; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 3.7e-71;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 IAQVSGKRAIAQVAASRSSEKVEYISEAMERVNDGYITIEESRGMELEVEGMDQ 192
DB 133 IAQVSGKRAIAQVAASRSSEKVEYISEAMERVNDGYITIEESRGMELEVEGMDQ 192
QY 193 FDRGYLSQYMTWTDNKNV 210
DB 193 FDRGYLSQYMTWTDNKNV 210

RESULT 14
069135 PRELIMINARY; PRT; 184 AA.
AC 069135;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (fragment).
GN Cpn60.
OS Streptococcus Iniae.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1346;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC29178;
RX MEDLINE-98313012; PubMed-9650992;
RA Goh S.H., Driedger D., Gillett S., Low D.E., Hemmingsen S.M., Amos M.,
RA Chan D., Lovgren M., Willey B.M., Shaw C., Smith J.A.;
RT Streptococcus Iniae, a human and animal pathogen: specific
RT identification by the chaperonin 60 gene identification method. *;
RL J. Clin. Microbiol. 36:2164-2166(1998).
DR EMBL: AF5746; 1SRV.
DR HSP: P45746; 1SRV.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
KM ATP-binding; Chaperone.
FT NON_TER 1
FT 184
SQ SEQUENCE 184 AA; 20009 MW; CE577F5CBA07E374 CRC64;

Query Match 13.8%; Score 75; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-68;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 AIAQVAASRSSEKVEYISEAMERVNDGYITIEESRGMELEVEGMDQFDRGYLSQY 201
DB 52 AIAQVAASRSSEKVEYISEAMERVNDGYITIEESRGMELEVEGMDQFDRGYLSQY 111
QY 202 MYTDNEMKVAADLENP 216
DB 112 MYTDNEMKVAADLENP 126

RESULT 15
09X4R5
ID 09X4R5 PRELIMINARY; PRT; 540 AA.
AC 09X4R5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
GN GROEL.
OS Streptococcus pneumoniae.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CP1200;
RA Kim S.N., Lee J.Y., Kim S.W., Choi I.H., Rhee D.K.;
RT *GroEL sequences in Streptococcus pneumoniae. *;
RL submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AF117741; AAD23455.1; -;
DR HSP: P06139; 1GRL.
DR InterPro: IPR001844; Chaperln_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PROSITE: PS00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONIN60_CPN60; 1.
KM ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 57213 MW; 4CDB489AF1C632DA CRC64;

Query Match 12.8%; Score 70; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 6.6e-63;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 NRRLIITADVDGEMLPVLNKRGTFFNVAVKAPGDRKKALMEDIALITGCVITIE 301
DB 242 NRRLIITADVDGEMLPVLNKRGTFFNVAVKAPGDRKKALMEDIALITGCVITIE 301
QY 302 DLGELKDAT 311
DB 302 DLGELKDAT 311

Search completed: April 8, 2003, 14:37:27
Job time : 103 secs